

In the Claims:

Please cancel claims 1-35. Please enter claims 36-75 as follows:

Claims 1-35 (cancelled)

36. (New) A method for the production of seeds, comprising the step of permitting pollination of a plant comprising a nucleic acid sequence effective for reducing levels of general DNA methylation, said nucleic acid sequence operably linked to a promoter, wherein seeds that develop on said plant have increased mean seed weight compared to the mean seed weight of seeds that develop on a corresponding pollinated plant that lacks said nucleic acid sequence.
37. (New) The method of claim 36, wherein said pollinated plant is a dicotyledonous plant.
38. (New) The method of claim 36, wherein said nucleic acid sequence is a transgene.
39. (New) The method of claim 38, wherein said nucleic acid sequence comprises an antisense sequence having at least 80% identity to DNA that encodes the *Arabidopsis* DNA methyltransferase 1 enzyme.
40. (New) The method of claim 38, wherein said nucleic acid sequence is a homologue of *Arabidopsis* DNA methyltransferase 1.
41. (New) The method of claim 40, wherein said nucleic acid sequence is transcribed into a double strand RNA.
42. (New) The method of claim 40, wherein said nucleic acid sequence comprises a sense sequence having at least 80% identity to DNA that encodes the *Arabidopsis* DNA methyltransferase 1 enzyme.
43. (New) The method of claim 36, wherein said seeds are viable.

44. (New) The method of claim 38, wherein said nucleic acid sequence is transcribed into a ribozyme effective for inactivating a DNA methyltransferase.
- 45 (New) The method of claim 36, wherein said promoter is a gynoecium-specific promoter.
46. (New) The method of claim 45, wherein said promoter is a female germ line promoter.
47. (New) The method of claim 36, wherein said pollination occurs with pollen that lacks said nucleic acid sequence.
48. (New) The method of claim 36, wherein seeds that develop on said pollinated plant have a mean seed weight that is at least 47% greater than the mean seed weight of seeds that develop on said corresponding plant that lacks said nucleic acid sequence.
49. (New) The method of claim 48, wherein seeds that develop on said pollinated plant have a mean seed weight that is at least 81% greater than the mean seed weight of seeds that develop on said corresponding plant that lacks said nucleic acid sequence.
50. (New) A transgenic plant containing a transgene comprising a nucleic acid sequence effective for reducing levels of general DNA methylation, said nucleic acid sequence operably linked to a gynoecium-specific promoter.
51. (New) The plant of claim 50, wherein said plant is a dicotyledonous plant.
52. (New) The plant of claim 50, wherein said nucleic acid sequence comprises an antisense sequence having at least 80% identity to DNA that encodes the *Arabidopsis* DNA methyltransferase 1 enzyme.

53. (New) The plant of claim 50, wherein said nucleic acid sequence is a homologue of the *Arabidopsis* DNA methyltransferase 1 enzyme.

54. (New) The plant of claim 53, wherein said nucleic acid sequence is transcribed into a double strand RNA.

55. (New) The plant of claim 53, wherein said nucleic acid sequence comprises a sense sequence having at least 80% identity to DNA that encodes the *Arabidopsis* DNA methyltransferase 1 enzyme.

56. (New) The plant of claim 50, wherein said nucleic acid sequence is transcribed into a ribozyme effective for inactivating a DNA methyltransferase.

57. (New) The plant of claim 50, wherein said gynoecium-specific promoter is a female germ line promoter.

58. (New) The plant of claim 50, wherein seeds that develop on said plant, after pollination by pollen that lacks said transgene, have a mean seed weight that is at least 47% greater than the mean seed weight of seeds that develop on a corresponding plant that lacks said nucleic acid sequence.

59. (New) The plant of claim 58, wherein said seeds are viable.

60. (New) The plant of claim 58, wherein seeds that develop on said plant, after pollination by pollen that lacks said transgene, have a mean seed weight that is at least 81% greater than the mean seed weight of seeds that develop on a corresponding plant that lacks said nucleic acid sequence.

61. (New) The plant of claim 60, wherein said seeds are viable.

62. (New) A method for the production of seeds, comprising the step of permitting self-pollination of a plant comprising a nucleic acid sequence effective for reducing levels of general DNA methylation, said nucleic acid sequence operably linked to gynoecium-specific promoter, wherein seeds that develop on said plant have increased mean seed weight compared to the mean seed weight of seeds that develop on a corresponding self-pollinated plant that lacks said nucleic acid sequence.
63. (New) The method of claim 62, wherein said plant is a dicotyledonous plant.
64. (New) The method of claim 62, wherein said nucleic acid sequence is a transgene.
65. (New) The method of claim 64, wherein said nucleic acid sequence comprises an antisense sequence having at least 80% identity to DNA that encodes the *Arabidopsis* DNA methyltransferase 1 enzyme.
66. (New) The method of claim 64, wherein said nucleic acid sequence is a homologue of *Arabidopsis* DNA methyltransferase 1.
67. (New) The method of claim 66, wherein said nucleic acid sequence is transcribed into a double strand RNA.
68. (New) The method of claim 66, wherein said nucleic acid sequence comprises a sense sequence having at least 80% identity to DNA that encodes the *Arabidopsis* DNA methyltransferase 1 enzyme.
69. (New) The method of claim 62, wherein said seeds are viable.
70. (New) The method of claim 62, wherein said nucleic acid sequence is transcribed into a ribozyme effective for inactivating a DNA methyltransferase.

71. (New) The method of claim 62, wherein said gynoecium-specific promoter is a female germ line promoter.

72. (New) The method of claim 62, wherein seeds that develop on said plant have a mean seed weight that is at least 47% greater than the mean seed weight of seeds that develop on a corresponding plant that lacks said nucleic acid sequence.

73. (New) The method of claim 72, wherein seeds that develop on said plant have a mean seed weight that is at least 81% greater than the mean seed weight of seeds that develop on a corresponding plant that lacks said nucleic acid sequence.